PATENT
Attorney Docket No. 018547-034800US
Client Ref.: 3079

#32

**IN THE UNITED STATES PATENT AND TRADEMARK OFFICE**

In re application of:

David H. Mack, et al.

Patent No. 6,420,108 B2

Issued: July 16, 2002

For: Computer-Aided Display for Comparative Gene Expression

Examiner: Jeffrey Siew

Art Unit: 1656

**Request for Certificate of Correction**



Commissioner for Patents
P.O. Box 1450
Alexandria, VA 22313-1450

Sir:

Pursuant to 37 CFR 1.322, counsel for Assignee submits a Certificate of Correction. Claim 6 was correctly presented by applicant in the amendment of August 15, 2000. However, the reference to claim 5 was apparently deleted in printing of the patent. No fee is required for this Certificate. The desired corrections are set forth on form PTO/SB/44, enclosed herewith.

Respectfully submitted,

Joe Liebeschuetz
Reg. No. 37,505

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JOL/sjj
60830304 v1

# UNITED STATES PATENT AND TRADEMARK OFFICE
# CERTIFICATE OF CORRECTION



PATENT NO. : US 6,420,108 B2

APPLICATION NO.: 09/020,743

ISSUE DATE : July 16, 2002

INVENTOR(S) : Mack, *et al.*

It is certified that an error appears or errors appear in the above-identified patent and that said Letters Patent is hereby corrected as shown below:

6. The method of claim 5, wherein said monitoring further comprises inputting a plurality of hybridization intensities from pairs of perfect match and mismatch probes, said perfect match probes being perfectly complementary to a target nucleic acid sequence indicative of expression of said selected gene and said mismatch probes having at least one base mismatch with said target sequence, and said hybridization intensities indicating hybridization affinity between said perfect match and mismatch probes and a sample nucleic acid sequence from said one of said samples; comparing the hybridization intensities of each pair of perfect match probe and mismatch probe; and generating said expression level for said expressed sequence and said one of said samples responsive to results of said comparing.

MAILING ADDRESS OF SENDER (Please do not use customer number below):

TOWNSEND AND TOWNSEND AND CREW LLP
Two Embarcadero Center, Eighth Floor
San Francisco, CA 94111-3834

Docket No. 018547-034800US

60830179 v1

UNITED STATES PATENT AND TRADEMARK OFFICE

# CERTIFICATE OF CORRECTION

PATENT NO. : 6,420,108 B2
APPLICATION NO. : 09/020743
DATED : July 16, 2002
INVENTOR(S) : Mack et al.



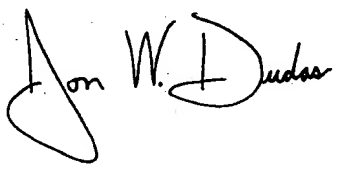
It is certified that error appears in the above-identified patent and that said Letters Patent is hereby corrected as shown below:

Column 15, line 50, claim 6 should read:

6. The method of claim 5, wherein said monitoring further comprises inputting a plurality of hybridization intensities from pairs of perfect match and mismatch probes, said perfect match probes being perfectly complementary to a target nucleic acid sequence indicative of expression of said selected gene and said mismatch probes having at least one base mismatch with said target sequence, and said hybridization intensities indicating hybridization affinity between said perfect match and mismatch probes and a sample nucleic acid sequence from said one of said samples; comparing the hybridization intensities of each pair of perfect match probe and mismatch probe; and generating said expression level for said expressed sequence and said one of said samples responsive to results of said comparing.

Signed and Sealed this

Seventeenth Day of October, 2006



JON W. DUDAS
*Director of the United States Patent and Trademark Office*

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# CERTIFICATE OF CORRECTION



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6. The method of claim 5, wherein said monitoring further comprises inputting a plurality of hybridization intensities from pairs of perfect match and mismatch probes, said perfect match probes being perfectly complementary to a target nucleic acid sequence indicative of expression of said selected gene and said mismatch probes having at least one base mismatch with said target sequence, and said hybridization intensities indicating hybridization affinity between said perfect match and mismatch probes and a sample nucleic acid sequence from said one of said samples; comparing the hybridization intensities of each pair of perfect match probe and mismatch probe; and generating said expression level for said expressed sequence and said one of said samples responsive to results of said comparing.

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